

FIGURE 1

1 GAACCAGCCT GCACGCGCTG GCTCCGGGTG ACAGCCGCGC GCCTCGGCCA
 51 GGATCTGAGT GATGAGACGT GTCCCCACTG AGGTGCCCCA CAGCAGCAGG
 101 TGTGTGAGCAT GGGCTGAGAA GCTGGACCGG CACCAAAGGG CTGGCAGAAA
 151 TGGGCGCCTG GCTGATTCTT AGGCAGTTGG CGGCAGCAAG GAGGAGAGGC
 201 CGCAGCTTCT GGAGCAGAGC CGAGACGAAG CAGTTCTGGA GTGCCTGAAC
 251 GGCCCCCTGA GCCCTACCCG CCTGGCCCAC TATGGTCCAG AGGCTGTGGG
 301 TGAGCCGCCT GCTGCGGCAC CGGAAAGCCC AGCTCTTGCT GGTCAACCTG
 351 CTAACCTTTG GCCTGGAGGT GTGTTTGGCC GCAGGCATCA CCTATGTGCC
 401 GCCTCTGCTG CTGGAAGTGG GGGTAGAGGA GAAGTTCATG ACCATGGTGC
 451 TGGGCATTGG TCCAGTGCTG GGCCTGGTCT GTGTCCCGCT CCTAGGCTCA
 501 GCCAGTGACC ACTGGCGTGG ACGCTATGGC CGCCGCCGGC CCTTCATCTG
 551 GGCAGTGTCC TTGGGCATCC TGCTGAGCCT CTTTCTCATC CCAAGGGCCG
 601 GCTGGCTAGC AGGGCTGCTG TGCCCGGATC CCAGGCCCCCT GGAGCTGGCA
 651 CTGCTCATCC TGGGCGTGGG GCTGCTGGAC TTCTGTGGCC AGGTGTGCTT
 701 CACTCCACTG GAGGCCCTGC TCTCTGACCT CTTCCGGGAC CCGGACCACT
 751 GTCGCCAGGC CTACTCTGTC TATGCCTTCA TGATCAGTCT TGGGGGCTGC
 801 CTGGGCTACC TCCTGCCTGC CATTGACTGG GACACCAGTG CCCTGGCCCC
 851 CTACCTGGGC ACCCAGGAGG AGTGCCTCTT TGGCCTGCTC ACCCTCATCT
 901 TCCTCACCTG CGTAGCAGCC AACTGCTGG TGGCTGAGGA GGCAGCGCTG
 951 GGCCCCACCG AGCCAGCAGA AGGGCTGTGC GCCCCCTCCT TGTCGCCCCA
 1001 CTGCTGTCCA TGCCGGGCCC GCTTGGCTTT CCGGAACCTG GGCGCCCTGC
 1051 TTCCCCGGCT GCACCAGCTG TGCTGCCGCA TGCCCCGCAC CCTGCGCCGG
 1101 CTCTTCGTGG CTGAGCTGTG CAGCTGGATG GCACTCATGA CCTTCACGCT
 1151 GTTTTACACG GATTTTCGTG GCGAGGGGCT GTACCAGGGC GTGCCCAGAG
 1201 CTGAGCCGGG CACCGAGGCC CGGAGACACT ATGATGAAGG CGTTCGGATG
 1251 GGCAGCCTGG GGCTGTTCTT GCAGTGCGCC ATCTCCCTGG TCTTCTCTCT
 1301 GGTCATGGAC CGGCTGGTGC AGCGATTGCG CACTCGAGCA GTCTATTTGG
 1351 CCAGTGTGGC AGCTTTCCCT GTGGCTGCCG GTGCCACATG CCTGTCCAC
 1401 AGTGTGGCCG TGGTGACAGC TTCAGCCGCC CTCACCGGGT TCACCTTCTC

FIGURE 1 – continued

1451 AGCCCTGCAG ATCCTGCCCT ACACACTGGC CTCCCTCTAC CACCGGGAGA
 1501 AGCAGGTGTT CCTGCCCAAA TACCGAGGGG ACACTGGAGG TGCTAGCAGT
 1551 GAGGACAGCC TGATGACCAG CTTCTTGCCA GGCCCTAAGC CTGGAGCTCC
 1601 CTTCCCTAAT GGACACGTGG GTGCTGGAGG CAGTGGCCTG CTCCACCTC
 1651 CACCCGCGCT CTGCGGGGCC TCTGCCTGTG ATGTCTCCGT ACGTGTGGTG
 1701 GTGGGTGAGC CCACCGAGGC CAGGGTGGTT CCGGGCCGGG GCATCTGCCT
 1751 GGACCTCGCC ATCCTGGATA GTGCCTTCCT GCTGTCCCAG GTGGCCCCAT
 1801 CCCTGTTTAT GGGCTCCATT GTCCAGCTCA GCCAGTCTGT CACTGCCTAT
 1851 ATGGTGTCTG CCGCAGGCCT GGGTCTGGTC GCCATTTACT TTGCTACACA
 1901 GGTAGTATTT GACAAGAGCG ACTTGCCAA AACTCAGCG TAGAAAACTT
 1951 CCAGCACATT GGGGTGGAGG GCCTGCCTCA CTGGGTCCCA GCTCCCCGCT
 2001 CCTGTTAGCC CCATGGGGCT GCCGGGCTGG CCGCCAGTTT CTGTTGCTGC
 2051 CAAAGTAATG TGGCTCTCTG CTGCCACCCT GTGCTGCTGA GGTGCGTAGC
 2101 TGCACAGCTG GGGGCTGGGG CGTCCCTCTC CTCTCTCCCC AGTCTCTAGG
 2151 GCTGCCTGAC TGGAGGCCTT CCAAGGGGGT TTCAGTCTGG ACTTATACAG
 2201 GGAGGCCAGA AGGGCTCCAT GCACTGGAAT GCGGGGACTC TGCAGGTGGA
 2251 TTACCCAGGC TCAGGGTTAA CAGCTAGCCT CCTAGTTGAG ACACACCTAG
 2301 AGAAGGGTTT TTGGGAGCTG AATAAACTCA GTCACCTGGT TTCCCATCTC
 2351 TAAGCCCCTT AACCTGCAGC TTCGTTTAAT GTAGCTCTTG CATGGGAGTT
 2401 TCTAGGATGA AACACTCCTC CATGGGATTT GAACATATGA AAGTTATTTG
 2451 TAGGGGAAGA GTCCTGAGGG GCAACACACA AGAACCAGGT CCCCTCAGCC
 2501 CACAGCACTG TCTTTTTGCT GATCCACCCC CCTCTTACCT TTTATCAGGA
 2551 TGTTGCCTGT TGGTCCTTCT GTTGCCATCA CAGAGACACA GGCATTTAAA
 2601 TATTTAACTT ATTTATTTAA CAAAGTAGAA GGAATCCAT TGCTAGCTTT
 2651 TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGGATCC CCAACAATCA
 2701 GGTCCTCTGA GATAGCTGGT CATTGGGCTG ATCATTGCCA GAATCTTCTT
 2751 CTCCTGGGGT CTGGCCCCC AAAATGCCTA ACCCAGGACC TTGGAAATTC
 2801 TACTCATCCC AAATGATAAT TCCAAATGCT GTTACCCAAG GTTAGGGTGT

FIGURE 1 - continued

2851 TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT CTCAACGGCT TCCCTAACCA
2901 CCCCTCTTCT CTTGGCCCAG CCTGGTTCCC CCCACTTCCA CTCCCCCTCTA
2951 CTCTCTCTAG GACTGGGCTG ATGAAGGCAC TGCCCCAAAAT TTCCCCCTACC
3001 CCCAACTTTC CCCTACCCCC AACTTTCCCC ACCAGCTCCA CAACCCTGTT
3051 TGGAGCTACT GCAGGACCAG AAGCACAAAG TGCGGTTTCC CAAGCCTTTG
3101 TCCATCTCAG CCCCCAGAGT ATATCTGTGC TTGGGGAATC TCACACAGAA
3151 ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG GAGGTCTTAT CTCTCAGGGG
3201 GGGGTTTAAG TGCCGTTTGC AATAATGTCG TCTTATTTAT TTAGCGGGGT
3251 GAATATTTTA TACTGTAAGT GAGCAATCAG AGTATAATGT TTATGGTGAC
3301 AAAATTAAAG GCTTCTTAT

FIGURE 2

1 MVQRLWVSRL LRHRKAQLLL VNLITFGLEV CLAAGITYVP PLLLEVGVVEE
51 KFMTMVLGIG PVLGLVCVPL LGSASDHWRG RYGRRRPFIW ALSLGILLSL
101 FLIPRAGWLA GLLCPDPRPL ELALLILGVG LLDFCGQVCF TPLEALLSDL
151 FRDPDHCRQA YSVYAFMISL GGCLGYLLPA IDWDTALAP YLGTQEECLF
201 GLLTLIFLTC VAATLLVAEE AALGPTEPAE GLSAPSLSPH CCPCRARLAF
251 RNLGALLPRL HQLCCRPRT LRRLFVAELC SWMALMTFTL FYTDFVGEGL
301 YQGVPRAPG TEARRHYDEG VRMGSLGLFL QCAISLVFSL VMDRLVQRFQ
351 TRAVYLASVA AFPVAAGATC LSHSVAVVTA SAALTGFTFS ALQILPYTLA
401 SLYHREKQVF LPKYRGDTGG ASSEDSLMTS FLPKPKPGAP FPNHVGAGG
451 SGLLPPPPAL CGASACDVSV RVVVGEPTEA RVVPGRGICL DLAILDSAFL
501 LSQVAPSLFM GSIVQLSQSV TAYMVSAAGL GLVAIYFATQ VVFDKSDLAK
551 YSA

FIGURE 3

DcSUT2 1 MENGTKELNKPQPPSSAAMQLQTPVQKIPTATWKLVLVAIAAGVQFGWA 50
PROST03 1MVQRLWVSRLLRHRKAQLLLLVNLLTFGLEVCLA 33
51 LQLSLLTPYVQLLGIPHKWAAYIWLCGPISGMLVQPIVGYYSDHCQSSFG 100
34 AGITYVPPLLLLEVGVEEKFMTMVLGIGPVLGLVCVPLLGSASDHWGRYG 83
101 RRRPFIASGAGCVAISVILIGFAADISYKAGDDMSKTLKPRAVTVFVIGF 150
84 RRRPFIWALSGLILLSLFLIPRAGWLAGLLCPDP...RPLELALLILGV 129
151 WILDVANNMLQGPCRALLADLCSGDTRMRSANAFYSFFMAVGNILGYAA 200
130 GLLDFCGQVCFTPLEALLSDLFR.DPDHCRQAYSVYAFMISLGGCLGYLL 178
201 GSYN.NLYKLFPPFSKTHACDLYCANLKSCFIISIALLIITVVALSVVRE 249
179 PAIDWDTALAPYLGTQEELFGLLTLIFLTCVAATLLVAEEAALGPTEP 228
250 NSGPPDDADAAEPPSSGKIPV..FGELLGALKDL...PRPMLLLLIIVT 293
229 AEGLSAPSLSPHCCPCRARLAFRNLGALLPRLHQLCCRMPRTLRLRFVAE 278
294 CLNWIAWFPFILFDTDWMGREIYGGT.....AGQKLYDQGVRAALGL 337
279 LCSWMALMTFTLFYTFVGEGLYQGVPRAEPTARRHYDEGVRMGSLGL 328
338 LLNSVVLGLTSLIAVEYLVRGVGVKILWGFVNFILAIGLVMTVVSKVAQ 387
329 FLQCAISLVFSLVMDRLVQRFQTRAV.....YLASVAAFPVAA 366
388 HQREHSANGQLLPPSAGVKAGALSLSILGIPLSITYSIPFALASIYSSG 437
367 GATCLSHSVAVVTASAALTGFTFSALQILPYTLASLYHREKQVFLPKYRG 416
438 SGAGQGLSLGVLNLAIVVPQMIVSVLAGPFDLSFGGGNLPAFVVGAISAA 487
417 DTGGASSEDLSMTSFLPGPKPGAPFPNGHVGAGGSGLLPPPPALCGASAC 466
488 ISGVLAIVLLPKPSKDAASKLSLSGTYH..... 515
467 DVSVRVVVGEPTARVVPGRGICLDLAILDSAFLLSQVAPSLFMGSIVQL 516

1000
900
800
700
600
500
400
300
200
100
0

FIGURE 4

GAACCAGCCTGCACGCGCTGGCTCCGGGTGACAGCCGCGCGCTCGGCCAGGATCTGAGT
 1 -----+-----+-----+-----+-----+-----+-----+ 60
 CTTGGTTCGGACGTGCGCGACCGAGGCCCACTGTGCGCGCGCGAGCCGGTCCTAGACTCA

GATGAGACGTGTCCCCACTGAGGTGCCCCACAGCAGCAGGTGTTGAGCATGGGCTGAGAA
 61 -----+-----+-----+-----+-----+-----+-----+ 120
 CTACTCTGCACAGGGGTGACTCCACGGGGTGTCTGTCGTCACAACTCGTACCCGACTCTT

GCTGGACCGGCACCAAAGGGCTGGCAGAAATGGGCGCCTGGCTGATTCCCTAGGCAGTTGG
 121 -----+-----+-----+-----+-----+-----+-----+ 180
 CGACCTGGCCGTGGTTTCCCGACCGTCTTTACCCGCGGACCGACTAAGGATCCGTCAACC

CGGCAGCAAGGAGGAGAGGCCGAGCTTCTGGAGCAGAGCCGAGACGAAGCAGTTCTGGA
 181 -----+-----+-----+-----+-----+-----+-----+ 240
 GCCGTCGTTCTCTCTCCGGCGTCGAAGACCTCGTCTCGGCTCTGCTTCGTCAAGACCT

GTGCCTGAACGGCCCCCTGAGCCCTACCCGCTGGCCCACTATGGTCCAGAGGCTGTGGG
 241 -----+-----+-----+-----+-----+-----+-----+ 300
 CACGGAATTGCCGGGGGACTCGGGATGGGCGGACCGGGTGATACCAGGTCTCCGACACCC

c M V Q R L W V -

TGAGCCGCTGCTGCGGCACCGGAAAGCCAGCTCTTGTCTGCTAACCTGCTAACCTTTG
 301 -----+-----+-----+-----+-----+-----+-----+ 360
 ACTCGGCGGACGACGCCGTGGCCTTTTCGGGTCGAGAACGACCACTTGGACGATTGGAAC

c S R L L R H R K A Q L L L V N L L T F G -

GCCTGGAGGTGTGTTTGGCCGAGGCATCACCTATGTGCCGCTCTGCTGTGGAAGTGG
 361 -----+-----+-----+-----+-----+-----+-----+ 420
 CGGACCTCCACACAAACCGGCGTCCGTAGTGATACACGGCGGAGACGACCTTCACC

c L E V C L A A G I T Y V P P L L L E V G -

GGGTAGAGGAGAAGTTTCATGACCATGGTGTCTGGGCATTGGTCCAGTGCTGGGCCTGGTCT
 421 -----+-----+-----+-----+-----+-----+-----+ 480
 CCCATCTCTCTTCAAGTACTGGTACCAGACCCGTAACCAGGTACGACCCGGACCGA

c V E E K F M T M V L G I G P V L G L V C -

GTGTCCCGCTCCTAGGCTCAGCCAGTGACCACTGGCGTGGACGCTATGGCCGCCGCCGGC
 481 -----+-----+-----+-----+-----+-----+-----+ 540
 CACAGGGCGAGGATCCGAGTCGGTCACTGGTGACCGCACCTGCGATACCGCGGCGGCCG

c V P L L G S A S D H W R G R Y G R R R P -

CCTTCATCTGGGCACTGTCTTGGGCATCCTGCTGAGCCTCTTTCTCATCCAAGGGCCG
 541 -----+-----+-----+-----+-----+-----+-----+ 600
 GGAAGTAGACCCGTGACAGGAACCCGTAGGACGACTCGGAGAAAGAGTAGGGTTCCTGGC

c F I W A L S L G I L L S L F L I P R A G -

GCTGGCTAGCAGGGTGTGTGCCCCGATCCCAGGCCCTGGAGCTGGCACTGCTCATCC
 601 -----+-----+-----+-----+-----+-----+-----+ 660
 CGACCGATCGTCCCGACGACACGGGCCTAGGGTCCGGGGACCTCGACCGTGACGAGTAGG

c W L A G L L C P D P R P L E L A L L I L -

TGGGCGTGGGGCTGCTGGACTTCTGTGGCCAGGTGTGCTTCACTCCACTGGAGGCCCTGC
 661 -----+-----+-----+-----+-----+-----+-----+ 720
 ACCCGCACCCCGACGACCTGAAGACACCGGTCCACACGAAGTGAGGTGACCTCCGGGACG

c G V G L L D F C G Q V C F T P L E A L L -

FIGURE 4 – continued

TCTCTGACCTCTTCCGGGACCCGGACCACTGTGCGCCAGGCCTACTCTGTCTATGCCTTCA
 721 -----+-----+-----+-----+-----+-----+-----+ 780
 AGAGACTGGAGAAGGCCCTGGGCCTGGTGACAGCGGTCCGGATGAGACAGATACGGAAGT
 C S D L F R D P D H C R Q A Y S V Y A F M -
 TGATCAGTCTTGGGGGCTGCCTGGGCTACCTCCTGCCTGCCATTGACTGGGACACCACTG
 781 -----+-----+-----+-----+-----+-----+ 840
 ACTAGTCAGAACCCCGACGGACCCGATGGAGGACGGACGGTAACTGACCCTGTGGTCAC
 C I S L G G C L G Y L L P A I D W D T S A -
 CCCTGGCCCCCTACCTGGGCACCCAGGAGGAGTGCCTCTTTGGCCTGCTCACCCCTCATCT
 841 -----+-----+-----+-----+-----+-----+ 900
 GGGACCGGGGATGGACCCGTGGGTCTCTCACGAGAAACCGACGAGTGGGAGTAGA
 C L A P Y L G T Q E E C L F G L L T L I F -
 TCCTCACCTGCGTAGCAGCCACACTGCTGGTGGCTGAGGAGGCAGCGTGGGCCCCACCG
 901 -----+-----+-----+-----+-----+-----+ 960
 AGGAGTGGACGCATCGTCGGTGTGACGACCACCGACTCCTCCGTCGCGACCCGGGTGGC
 C L T C V A A T L L V A E E A A L G P T E -
 AGCCAGCAGAAGGGCTGTGCGCCCCCTCTTGTGCGCCCACTGCTGTCCATGCCGGGCCC
 961 -----+-----+-----+-----+-----+-----+ 1020
 TCGGTCTGTCTTCCCGACAGCCGGGGAGGAACAGCGGGGTGACGACAGGTACGGCCCCGG
 C P A E G L S A P S L S P H C C P C R A R -
 GCTTGGCTTTCCGGAACCTGGGCGCCCTGCTTCCCCGGCTGCACCAGCTGTGCTGCCGCA
 1021 -----+-----+-----+-----+-----+-----+ 1080
 CGAACCAGAAAGGCTTGGACCCGCGGGACGAAGGGGCGACGTGGTTCGACACGACGGCGT
 C L A F R N L G A L L P R L H Q L C C R M -
 TGCCCCGCACCCTGCGCCGGCTCTTCGTGGCTGAGCTGTGCAGCTGGATGGCACTCATGA
 1081 -----+-----+-----+-----+-----+-----+ 1140
 ACGGGGCGTGGGACGCGGCCGAGAAGCACCAGCTCGACACGTCGACCTACCGTGAGTACT
 C P R T L R R L F V A E L C S W M A L M T -
 CCTTCACGCTGTTTACACGGATTTTCGTGGGCGAGGGGCTGTACCAGGGCGTGCCAGAG
 1141 -----+-----+-----+-----+-----+-----+ 1200
 GGAAGTGCAGACAAAATGTGCCTAAAGCACCCGCTCCCCGACATGGTCCCGCACGGGTCTC
 C F T L F Y T D F V G E G L Y Q G V P R A -
 CTGAGCCGGGCACCGAGGCCCGGAGACACTATGATGAAGGCGTTCGGATGGGCAGCCTGG
 1201 -----+-----+-----+-----+-----+-----+ 1260
 GACTCGGCCCCGTGGCTCCGGGCTCTGTGATACTACTCCGCAAGCCTACCCGTCCGACC
 C E P G T E A R R H Y D E G V R M G S L G -
 GGCTGTTCCTGCACTGCGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACCGGCTGGTGC
 1261 -----+-----+-----+-----+-----+-----+ 1320
 CCCACAAGGACGTACGCGGTAGAGGGACCAAGAGAGACCAGTACCTGGCCGACCACG
 C L F L Q C A I S L V F S L V M D R L V Q -
 AGCGATTCCGCACTCGAGCAGTCTATTTGGCCAGTGTGGCAGCTTCCCTGTGGCTGCCG
 1321 -----+-----+-----+-----+-----+-----+ 1380
 TCGCTAAGCCGTGAGCTCGTCAGATAAACCGGTACACCGTCGAAAGGGACACCGACGGC
 C R F G T R A V Y L A S V A A F P V A A G -

FIGURE 4 - continued

GTGCCACATGCCTGTCCCACAGTGTGGCCGTGGTGACAGCTTCAGCCGCCCTCACCGGGT
 1381 -----+-----+-----+-----+-----+ 1440
 CACGGTGTACGGACAGGGTGTACACCGGCACCACTGTGGAAGTCGGCGGGAGTGGCCCA
 C A T C L S H S V A V V T A S A A L T G F -
 TCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCTCCCTCTACCACCGGGAGA
 1441 -----+-----+-----+-----+-----+ 1500
 ACTGGAAGAGTCGGGACGTCTAGGACGGGATGTGTGACCGGAGGGAGATGGTGGCCCTCT
 C T F S A L Q I L P Y T L A S L Y H R E K -
 AGCAGGTGTTCTGCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCC
 1501 -----+-----+-----+-----+-----+ 1560
 TCGTCCACAAGGACGGGTTTATGGCTCCCTGTGACCTCCACGATCGTCACTCCTGTCCG
 C Q V F L P K Y R G D T G G A S S E D S L -
 TGATGACCAGCTTCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGGACACGTGG
 1561 -----+-----+-----+-----+-----+ 1620
 ACTACTGGTCTGAAGGACGGTCCGGGATTCTGGACCTCGAGGAAGGGATTACCTGTGCACC
 C M T S F L P G P K P G A P F P N G H V G -
 GTGCTGGAGGCAGTGGCCTGTCTCCACCTCCACCCGCGCTCTGCGGGGCCCTCTGCCTGTG
 1621 -----+-----+-----+-----+-----+ 1680
 CACGACCTCCGTACCGGACGAGGGTGGAGGTGGGCGCGAGACGCCCCGAGACGGACAC
 C A G G S G L L P P P P A L C G A S A C D -
 ATGTCTCCGTACGTGTGGTGGGTGAGCCACCGAGGCCAGGGTGGTTCCGGGCCCGG
 1681 -----+-----+-----+-----+-----+ 1740
 TACAGAGGCATGCACACCACCACCACTCGGGTGGCTCCGGTCCACCAAGGCCCGGCC
 C V S V R V V V G E P T E A R V V P G R G -
 GCATCTGCCTGGACCTCGCCATCCTGGATAGTGCCTTCTGTCTGCCAGGTGGCCCCAT
 1741 -----+-----+-----+-----+-----+ 1800
 CGTAGACGGACCTGGAGCGGTAGGACCTATCACGGAAGGACGACAGGGTCCACCGGGGTA
 C I C L D L A I L D S A F L L S Q V A P S -
 CCCTGTTTATGGGCTCCATTGTCCAGCTCAGCCAGTCTGTCACTGCCTATATGGTGTCTG
 1801 -----+-----+-----+-----+-----+ 1860
 GGGACAAATACCCGAGGTAACAGGTCGAGTCGGTCAGACAGTGACGGATATACCACAGAC
 C L F M G S I V Q L S Q S V T A Y M V S A -
 CCGCAGGCCTGGGTCTGGTCGCCATTTACTTTGCTACACAGGTAGTATTTGACAAGAGCG
 1861 -----+-----+-----+-----+-----+ 1920
 GGCGTCCGGACCCAGACCAGCGGTAAATGAAACGATGTGTCCATCATAAACTGTTCTCGC
 C A G L G L V A I Y F A T Q V V F D K S D -
 ACTTGGCCAAATACTCAGCGTAGAAAACCTCCAGCACATTGGGGTGGAGGGCCTGCCTCA
 1921 -----+-----+-----+-----+-----+ 1980
 TGAACCGGTTTATGAGTCGCATCTTTGAAGTCTGTGTAACCCACCTCCCGGACGGAGT
 C L A K Y S A *
 CTGGGTCACAGCTCCCGCTCCTGTAGCCCCATGGGGCTGCGGGCTGGCCGCCAGTTT
 1981 -----+-----+-----+-----+-----+ 2040
 GACCCAGGGTCGAGGGGCGAGGACAATCGGGGTACCCCGACGGCCCGACCGGCGGTCAAA

FIGURE 4 - continued

2041 CTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCTGTGCTGCTGAGGTGCGTAGC 2100
 -----+-----+-----+-----+-----+-----+-----+
 GACAACGACGGTTTCATTACACCGAGAGACGACGGTGGGACACGACGACTCCACGCATCG

 2101 TGCACAGCTGGGGGCTGGGGCGTCCCTCTCTCTCTCCCCAGTCTCTAGGGCTGCCTGAC 2160
 -----+-----+-----+-----+-----+-----+-----+
 ACGTGTGCGACCCCCGACCCCGCAGGGAGAGGAGAGAGGGGTGAGAGATCCCGACGGACTG

 2161 TGGAGGCCTTCCAAGGGGGTTTCAGTCTGGACTTATACAGGGAGGCCAGAAGGGCTCCAT 2220
 -----+-----+-----+-----+-----+-----+-----+
 ACCTCCGGAAGGTTCCCCCAAAGTCAGACCTGAATATGTCCCTCCGGTCTTCCCGAGGTA

 2221 GCACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGGTTAACAGCTAGCCT 2280
 -----+-----+-----+-----+-----+-----+-----+
 CGTGACCTTACGCCCCTGAGACGTCCACCTAATGGGTCCGAGTCCCAATTGTGATCGGA

 2281 CCTAGTTGAGACACACCTAGAGAAGGGTTTTTGGGAGCTGAATAAACTCAGTCACCTGGT 2340
 -----+-----+-----+-----+-----+-----+-----+
 GGATCAACTCTGTGTGATCTCTTCCCAAAACCTCGACTTATTTGAGTCAGTGGACCA

 2341 TTCCCATCTCTAAGCCCCTTAACCTGCAGCTTCGTTTAAATGTAGCTCTTGCATGGGAGTT 2400
 -----+-----+-----+-----+-----+-----+-----+
 AAGGGTAGAGATTCGGGGAATTGGACGTGGAAGCAAATTACATCGAGAACGTACCCTCAA

 2401 TCTAGGATGAAACACTCCTCCATGGGATTTGAACATATGAAAGTTATTTGTAGGGGAAGA 2460
 -----+-----+-----+-----+-----+-----+-----+
 AGATCCTACTTTGTGAGGAGGTACCCTAAACTTGTATACTTTCAATAAACATCCCCTTCT

 2461 GTCCTGAGGGGCAACACACAAGAACCAGGTCCCCTCAGCCCACAGCACTGTCTTTTGTCT 2520
 -----+-----+-----+-----+-----+-----+-----+
 CAGGACTCCCCGTTGTGTGTTCTTGGTCCAGGGGAGTCGGGTGTCGTGACAGAAAAACGA

 2521 GATCCACCCCCCTCTTACCTTTTATCAGGATGTGGCCTGTTGGTCTTCTGTTGCCATCA 2580
 -----+-----+-----+-----+-----+-----+-----+
 CTAGGTGGGGGGAGAATGGAATAATAGTCCTACACCGGACAACCAGGAAGACAACGGTAGT

 2581 CAGAGACACAGGCATTTAAATATTTAACTTATTTATTTAAACAAAGTAGAAGGAATCCAT 2640
 -----+-----+-----+-----+-----+-----+-----+
 GTCTCTGTGTCCGTAAATTTATAAATTGAATAAATAAATTGTTTCATCTTCCCTTAGGTA

 2641 TGCTAGCTTTTCTGTGTTGGTGTCTAATATTTGGGTAGGGTGGGGGATCCCCAACAATCA 2700
 -----+-----+-----+-----+-----+-----+-----+
 ACGATCGAAAAGACACAACCACAGATTATAAACCCATCCCACCCCTAGGGGTGTTAGT

 2701 GGTCCCCTGAGATAGCTGGTCATTGGGCTGATCATTGCCAGAATCTTCTTCTCCTGGGGT 2760
 -----+-----+-----+-----+-----+-----+-----+
 CCAGGGGACTCTATCGACCAGTAACCCGACTAGTAACGGTCTTAGAAGAAGAGGACCCCA

 2761 CTGGCCCCCAAAATGCCTAACCCAGGACCTTGGAATTTCTACTCATCCCAAATGATAAT 2820
 -----+-----+-----+-----+-----+-----+-----+
 GACCGGGGGGTTTACGGATTGGGTCTGGAACCTTTAAGATGAGTAGGGTTTACTATTA

 2821 TCCAAATGCTGTTACCCAAGGTTAGGGTGTGAAGGAAGGTAGAGGTGGGGCTTCAGGT 2880
 -----+-----+-----+-----+-----+-----+-----+
 AGGTTTACGACAATGGGTTCCAATCCCACAACCTCCTTCCATCTCCCACCCGAGTCCA

 2881 CTCAACGGCTTCCCTAACCCACCCCTCTTCTCTTGGCCCAGCCTGGTTCCCCCACTTCCA 2940
 -----+-----+-----+-----+-----+-----+-----+
 GAGTTGCCGAAGGGATTGGTGGGGAGAAGAGAACCGGGTCGGACCAAGGGGGGTGAAGGT

 2941 CTCCCCTCTACTCTCTCTAGGACTGGGCTGATGAAGGCACTGCCCAAATTTCCCCTACC 3000
 -----+-----+-----+-----+-----+-----+-----+
 GAGGGGAGATGAGAGAGATCCTGACCCGACTACTTCCGTGACGGGTTTAAAGGGGATGG

FIGURE 4 - continued

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3001  CCCAACTTTCCCTACCCCCAACTTTCCCCACCAGCTCCACAACCCTGTTTGGAGCTACT
-----+-----+-----+-----+-----+-----+ 3060
GGGTTGAAAGGGGATGGGGGTGAAAGGGGTGGTCGAGGTGTTGGGACAAACCTCGATGA

3061  GCAGGACCAGAAGCACAAAGTGCGGTTTCCCAAGCCTTGTCCATCTCAGCCCCCAGAGT
-----+-----+-----+-----+-----+-----+ 3120
CGTCCTGGTCTTCGTGTTTACGCCAAAGGGTTCGGAAACAGGTAGAGTCGGGGGTCTCA

3121  ATATCTGTGCTTGGGGAATCTCACACAGAACTCAGGAGCACCCCCTGCCTGAGCTAAGG
-----+-----+-----+-----+-----+-----+ 3180
TATAGACACGAACCCCTTAGAGTGTGTCTTTGAGTCCTCGTGGGGGACGGACTCGATTCC

3181  GAGGTCTTATCTCTCAGGGGGGGGTTTAAAGTGCCGTTTGCAATAATGTCGTCTTATTTAT
-----+-----+-----+-----+-----+-----+ 3240
CTCCAGAATAGAGAGTCCCCCCCCAAATTACGGCAAACGTTATTACAGCAGAATAAATA

3241  TTAGCGGGGTGAATATTTTATACTGTAAGTGAGCAATCAGAGTATAATGTTTATGGTGAC
-----+-----+-----+-----+-----+-----+ 3300
AATCGCCCCACTTATAAAATATGACATTCAGTCGTTAGTCTCATATTACAAATACCACTG

3301  AAAATTAAAGGCTTTCTTAT
-----+-----+ 3320
TTTTAATTTCCGAAAGAATA

```

Figure 5
Expression of Prost 3 in Human Tissue

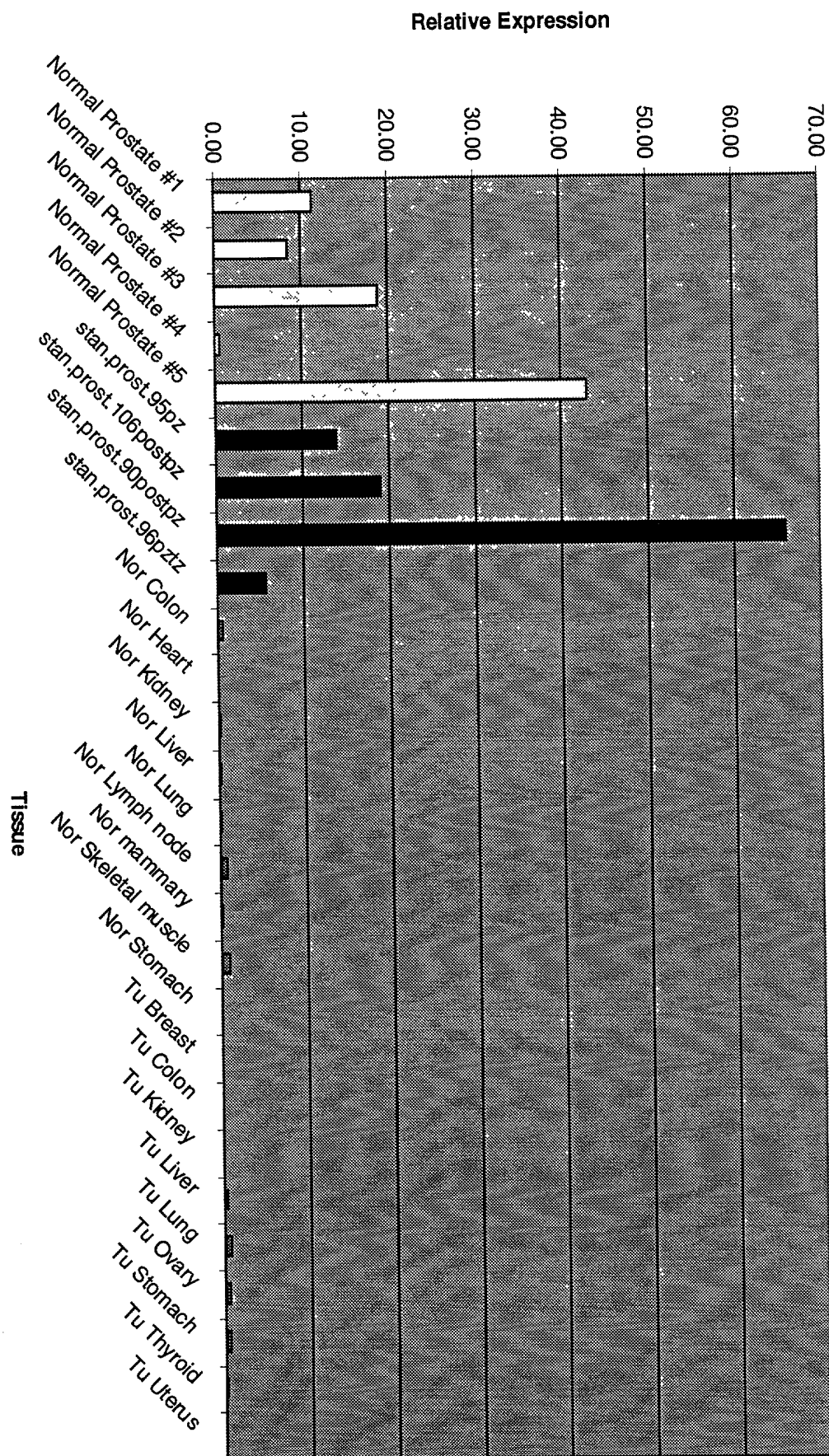
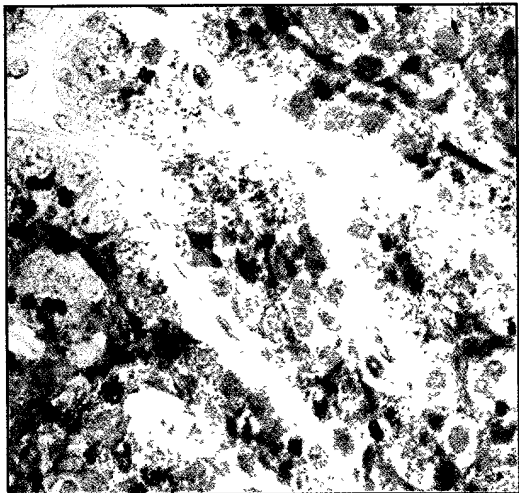


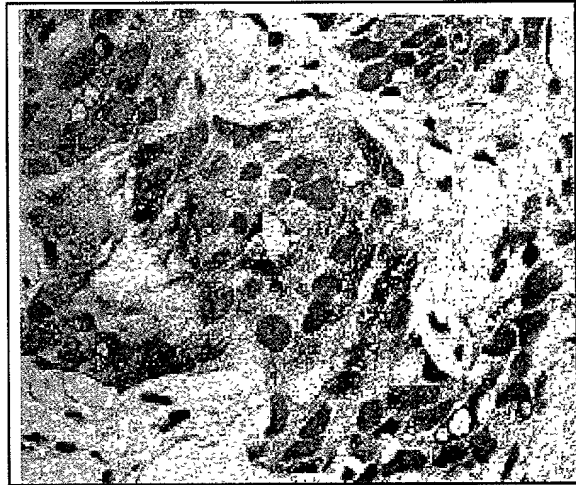
Fig. 6: Immunohistochemical staining of PROST 03 expression: PROST 03 expressing cells are shown in red.



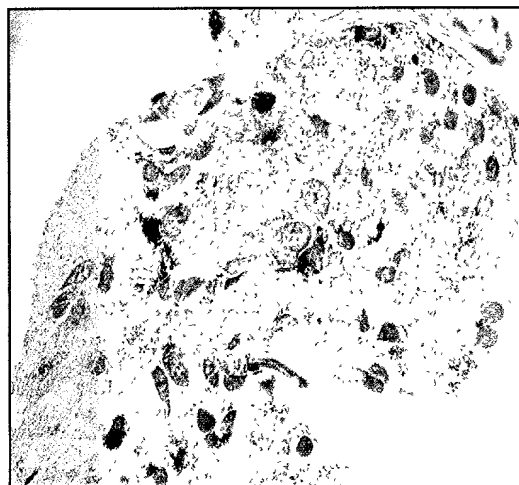
6a: Normal Prostate



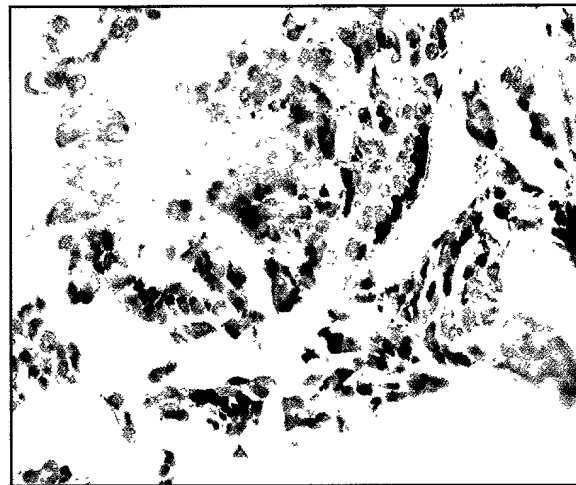
6b: Prostate Carcinoma



6c: Lymph Node, Metastatic Prostate Carcinoma



6d: Bone Marrow, Metastatic Prostate Carcinoma



6e: Bone, Metastatic Prostate Carcinoma